TOPIC 4

DNA, genes, chromosomes and protein synthesis

Pack 1

Q1.(a) Explain how the structure of DNA is related to its functions.

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(Extra space) ....

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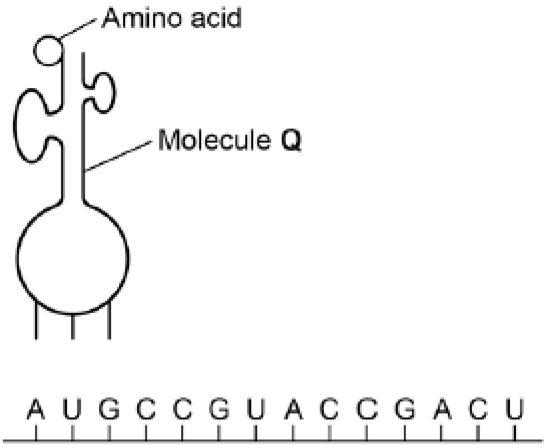
(6)

(Total 6 marks)

Q2. The diagram below represents one process that occurs during protein synthesis.



(a) Name the process shown.

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(1)

(b) Identify the molecule labelled **Q**.

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(1)

(c) In the diagram above, the first codon is AUG. Give the base sequence of:

the complementary DNA base sequence ....

the missing anticodon ....

The table below shows the base triplets that code for two amino acids.

Amino acid	**Encoding base triplet**
Aspartic acid	GAC, GAU
Proline	CCA, CCG, CCC, CCU

(2)

(d) Aspartic acid and proline are both amino acids. Describe how two amino acids differ from one another. You may use a diagram to help your description.

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(1)

(e) Deletion of the sixth base (G) in the sequence shown in the diagram above would change the nature of the protein produced but substitution of the same base would not. Use the information in the table and your own knowledge to explain why.

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(Extra space) ....

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(3)

(Total 8 marks)

Q3.(a) Messenger RNA (mRNA) is used during translation to form polypeptides.
Describe how mRNA is produced in the nucleus of a cell.

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(6)

(b) Describe the structure of proteins.

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(5)

(Total 11 marks)

Q4.(a) Genes for antibiotic resistance can be transmitted between bacteria. **Table 1** shows features of gene transmission.

Complete **Table 1** by putting a tick in the box if the statement is correct for vertical or horizontal gene transmission.

Table 1

Statement	**Vertical gene transmission**	**Horizontal gene transmission**
Gene is replicated		
Gene can be passed to other species of bacteria		
Involves conjugation		

(2)

(b) (i) The antibiotic tetracycline binds to ribosomes in bacterial cells.

Explain how this causes the death of bacterial cells.

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(2)

Scientists determined the amino acid sequences of two forms of a protein, **A** and **B**, found in two types of the same species of bacterium. They used these amino acid sequences to find the DNA base sequences that code for these proteins.

Table 2 shows their results for the same region of proteins **A** and **B**.

Table 3 shows DNA triplets that code for different amino acids.

Table 2

Protein A							
Amino acid sequence	Lys	Ser	Pro	Cys	Leu	Gly	Ala
DNA base sequence	TTT	TCA	GGT	ACG	GAA	CCA	CGA

Protein B							
Amino acid sequence	Lys	Ser	Pro	Trp	Pro	Trp	Cys
DNA base sequence	TTT	TCA	GGT				

Table 3

Amino acid	**DNA bases that code for this amino acid**
Trp	ACC
Pro	GGT or GGA
Cys	ACA or ACG

The amino acid sequence of protein **B** was the result of a mutation. A single base was added within the DNA sequence coding for protein **A**.

(ii) Use the information provided to complete the DNA base sequence that codes for protein **B**.

(1)

(iii) Complete the box to show which DNA base was added.

☐

(1)

(iv) Tetracycline can enter a bacterium through protein **A**. This protein is found in the plasma membrane.

Suggest how a change in the amino acid sequence of this protein could make a bacterium resistant to tetracycline.

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(2)
(Total 8 marks)

Q5.(a) (i) Why is the genetic code described as being universal?

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(1)

(ii) The genetic code uses four different DNA bases. What is the maximum number of different DNA triplets that can be made using these four bases?

(1)

Transcription of a gene produces pre-mRNA.

(b) Name the process that removes base sequences from pre-mRNA to form mRNA.

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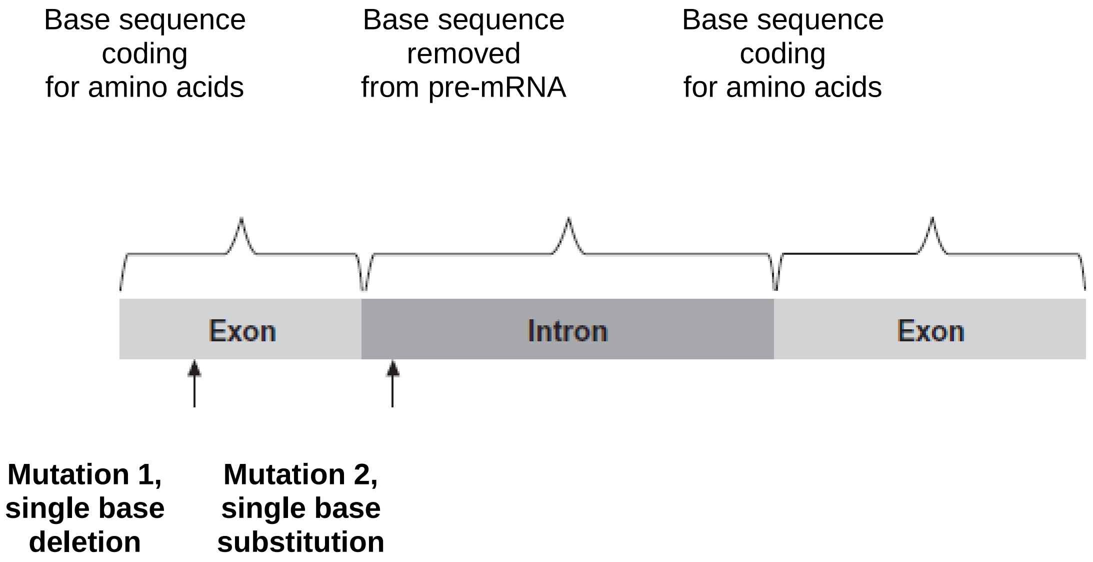
(1)

(c) The figure below shows part of a pre-mRNA molecule. Geneticists identified two mutations that can affect this pre-mRNA, as shown in the figure.


Base sequence coding for amino acids
Base sequence removed from pre-mRNA
Base sequence coding for amino acids
Exon
Intron
Exon
Mutation 1, single base deletion
Mutation 2, single base substitution

(i) **Mutation 1** leads to the production of a non-functional protein.

Explain why.

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(Extra space) ....

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(3)

(ii) What effect might **mutation 2** have on the protein produced?

Explain your answer.

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(2)

(Total 8 marks)

Q6.(a) The genetic code is described as being degenerate. What does this mean?

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(1)

(b) What is a codon?

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(2)

(c) (i) What is the role of RNA polymerase during transcription?

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(1)

(ii) mRNA can be converted to cDNA.

Name the enzyme used in this process.

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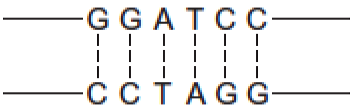
(1)

(d) The diagram shows the base sequence on DNA where a restriction endonuclease cuts DNA.



Use evidence from the diagram to explain what is meant by a palindromic recognition sequence on DNA.

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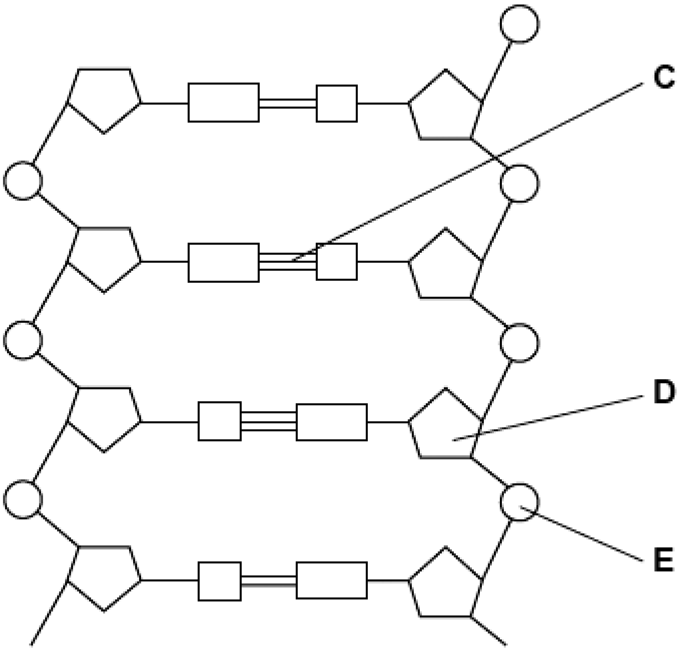
(1)
(Total 6 marks)

Q7. The diagram shows part of a DNA molecule.



(a) (i) DNA is a polymer. What is the evidence from the diagram that DNA is a polymer?

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(1)

(ii) Name the parts of the diagram labelled **C**, **D** and **E**.

Part **C** ....

Part **D** ....

Part **E** ....

(3)

(iii) In a piece of DNA, 34% of the bases were thymine.

Complete the table to show the names and percentages of the other bases.

Name of base	Percentage
Thymine	34
	34

(2)

(b) A polypeptide has 51 amino acids in its primary structure.

(i) What is the minimum number of DNA bases required to code for the amino acids in this polypeptide?

(1)

(ii) The gene for this polypeptide contains more than this number of bases.

Explain why

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(1)
(Total 8 marks)

Q8. The black mamba is a poisonous snake. Its poison contains a toxin.

The table shows the base sequence of mRNA that codes for the first two amino acids of this toxin.

Base sequence of anticodon on tRNA						
Base sequence of mRNA	**A**	**C**	**G**	**A**	**U**	**G**
Base sequence of DNA						

Complete the table to show

(a) (i) the base sequence of the anticodon on the first tRNA molecule that would bind to this mRNA sequence

(1)

(ii) the base sequence of the DNA from which this mRNA was transcribed

(1)

(b) The length of the section of DNA that codes for the complete toxin is longer than the mRNA used for translation. Explain why.

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(1)

(c) A mutation in the base sequence of the DNA that codes for the toxin would change the base sequence of the mRNA.

Explain how a change in the base sequence of the mRNA could lead to a change in the tertiary structure of the toxin.

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(1)

(d) The black mamba's toxin kills prey by preventing their breathing. It does this by inhibiting the enzyme acetylcholinesterase at neuromuscular junctions. Explain how this prevents breathing.

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(Extra space) ....

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(3)

(Total 7 marks)

Q9. The diagram shows a short sequence of DNA bases.

T T T G T A T A C T A G T C T A C T T C G T T A A T A

(a) (i) What is the maximum number of amino acids for which this sequence of DNA bases could code?

☐

(1)

(ii) The number of amino acids coded for could be fewer than your answer to part (a)(i).

Give **one** reason why.

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(1)

(b) Explain how a change in the DNA base sequence for a protein may result in a change in the structure of the protein.

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(Extra space) ....

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(3)

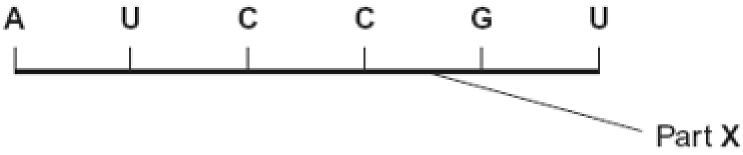
(c) A piece of DNA consisted of 74 base pairs. The two strands of the DNA, strands **A** and **B**, were analysed to find the **number** of bases of each type that were present. Some of the results are shown in the table.

	Number of bases			
	C	G	A	T
Strand **A**	26			
Strand **B**	19		9	

Complete the table by writing in the missing values.

(2)
(Total 7 marks)

Q10. The diagram shows part of a pre-mRNA molecule.



(a) (i) Name the **two** substances that make up part **X**.

.... and ....

(1)

(ii) Give the sequence of bases on the DNA strand from which this pre-mRNA has been transcribed.

....

(1)

(b) (i) Give one way in which the structure of an mRNA molecule is different from the structure of a tRNA molecule.

....

....

(1)

(ii) Explain the difference between pre-mRNA and mRNA.

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....

(1)

(c) The table shows the percentage of different bases in two pre-mRNA molecules. The molecules were transcribed from the DNA in different parts of a chromosome.

Part of chromosome	**Percentage of base**			
	A	**G**	**C**	**U**
Middle	38	20	24	
End	31	22	26	

(i) Complete the table by writing the percentage of uracil (U) in the appropriate boxes.

(1)

(ii) Explain why the percentages of bases from the middle part of the chromosome and the end part are different.

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(2)

(Total 7 marks)

Q11. (a) What name is used for the non-coding sections of a gene?

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(1)

Figure 1 shows a DNA base sequence. It also shows the effect of two mutations on this base sequence. **Figure 2** shows DNA triplets that code for different amino acids.

Figure 1

Original DNA base sequence	A	T	T	G	G	C	G	T	G	T	C	T
Amino acid sequence												
Mutation **1** DNA base sequence	A	T	T	G	G	A	G	T	G	T	C	T
Mutation **2** DNA base sequence	A	T	T	G	G	C	C	T	G	T	C	T

Figure 2

DNA triplets	**Amino acid**
GGT, GGC, GGA, GGG	Gly
GTT, GTA, GTG, GTC	Val
ATC, ATT, ATA	Ile
TCC, TCT, TCA, TCG	Ser
CTC, CTT, CTA, CTG	Leu

(b) Complete **Figure 1** to show the sequence of amino acids coded for by the original DNA base sequence.

(1)

(c) Some gene mutations affect the amino acid sequence. Some mutations do not. Use the information from **Figure 1** and **Figure 2** to explain

(i) whether mutation **1** affects the amino acid sequence

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(2)

(ii) how mutation **2** could lead to the formation of a non-functional enzyme.

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(3)

(d) Gene mutations occur spontaneously.

(i) During which part of the cell cycle are gene mutations most likely to occur?

....

(1)

(ii) Suggest an explanation for your answer.

....

....

(1)
(Total 9 marks)

M1.(a) 1. Sugar-phosphate (backbone) / double stranded / helix **so** provides strength / stability / protects bases / protects hydrogen bonds;

Must be a direct link / obvious to get the mark

Neutral: reference to histones

2. Long / large molecule **so** can store lots of information;

3. Helix / coiled **so** compact;

Accept: can store in a small amount of space for 'compact'

4. Base sequence allows information to be stored / base sequence codes for amino acids / protein;

Accept: base sequence allows transcription

5. Double stranded **so** replication can occur semi-conservatively / strands can act as templates / complementary base pairing / A-T and G-C so accurate replication / identical copies can be made;

6. (Weak) hydrogen bonds **for** replication / unzipping / strand separation / many hydrogen bonds **so** stable / strong;

Accept: 'H-bonds' for 'hydrogen bonds'

6

[6]

M2.(a) Translation;

1

(b) Transfer RNA / tRNA;

1

(c) TAC;

UAC;

2

(d) Have different R group;

Accept in diagram

1

(e) 1. Substitution would result in CCA / CCC / CCU;

2. (All) code for same amino acid / proline;

3. Deletion would cause frame shift / change in all following codons / change next codon from UAC to ACC;

3

[8]

M3.(a) 1. Helicase;

2. Breaks hydrogen bonds;

3. Only one DNA strand acts as template;

4. RNA nucleotides attracted to exposed bases;

5. (Attraction) according to base pairing rule;

6. RNA polymerase joins (RNA) nucleotides together;

7. Pre-mRNA spliced to remove introns;

6 max

(b) 1. Polymer of amino acids;

2. Joined by peptide bonds;

3. Formed by condensation;

4. Primary structure is order of amino acids;

5. Secondary structure is folding of polypeptide chain due to hydrogen bonding;

   Accept alpha helix / pleated sheet

6. Tertiary structure is 3-D folding due to hydrogen bonding and ionic / disulfide bonds;

7. Quaternary structure is two or more polypeptide chains;

5 max

[11]

M4.(a)

Statement	**Vertical**	**Horizontal**
Gene is replicated	✓	✓
Gene can be passed to other species of bacteria		✓
Involves conjugation		✓

*One mark for each correct **column***

2

(b) (i) 1. Prevents protein synthesis;

Accept: ribosomes produce proteins / chains of amino acids / polypeptides

Reject: ribosomes produce amino acids

2. (So) enzymes not produced / any named process involving proteins / enzymes is inhibited;

Accept: no (DNA) replication

Accept: cannot form a cell wall

Reject: no mitosis

Neutral: no growth / repair

2

(ii) **ACC GGA ACC ACG;**

1

(iii) **C;**

Accept: 'cytosine'

1

(iv) 1. Different tertiary structure / tertiary shape;

Neutral: 3D structure

2. (So tetracycline) does not fit / bind / is not complementary / does not enter / pass through (protein / into cell);

***Q** Reject: any reference to 'active site', 'enzyme-substrate complex' or (tetracycline) not fitting / binding to an enzyme*

Accept: (so) more tetracycline pumped out of cell

2

[8]

M5.(a) (i) (In all organisms / DNA,) the same triplet codes for the same amino acid;

Accept codon / same three bases / nucleotides

Accept plurals if both triplets and amino acids

Reject triplets code for an amino acid

Reject reference to producing amino acid

1

(ii) 64;

1

(b) Splicing;

Ignore deletion references

Accept RNA splicing

1

(c) (i)

1. (Mutation) changes triplets / codons after that point / causes frame shift;

   Accept changes splicing site

   Ignore changes in sequence of nucleotides / bases

2. Changes amino acid sequence (after this) / codes for different amino acids (after this);

   Accept changes primary structure

   Reject changes amino acid formed / one amino acid changed

3. Affects hydrogen / ionic / sulfur bond (not peptide bond);

4. Changes tertiary structure of protein (so non-functional);

   Neutral 3-D structure

3 max

(ii)

1. Intron non-coding (DNA) / only exons coding;

   Context is the ***intron***

Do not mix and match from alternatives

Neutral references to introns removed during splicing

1.and 2. Ignore ref. to code degenerate and get same / different amino acid in sequence

2. (So) not translated / no change in mRNA produced / no effect (on protein) / no effect on amino acid sequence;

   Accept does not code for amino acids

OR

3. Prevents / changes splicing;
4. (So) faulty mRNA formed;

   Accept exons not joined together / introns not removed
5. Get different amino acid sequence;

2 max

[8]

M6.(a) One / an amino acid (can be) coded for by more than one triplet;

Accept codon for triplet

Accept description of triplet − three bases / nucleotides

1

(b) 1. Triplet / three bases on mRNA;

1. Accept nucleotide for base

1. Accept DNA for mRNA

1. Ignore references to RNA unqualified

2. That code for an amino acid;

2. Accept code for stop / start

2

(c) (i) To join nucleotides together to form mRNA / premRNA / RNA;

Reject forming base pairs

Accept checking and correcting mismatched base pairs

1

(ii) Reverse transcriptase;

If they give two enzymes, no mark

1

(d) GGATCC same as CCTAGG in opposite direction;

Accept reads same both ways / same forward and back

Neutral bases are the opposite of each other / reference to base pairs

1

[6]

M7.(a) (i) Repeating units / nucleotides / monomer / molecules;

Allow more than one, but reject two

1

(ii) 1. C = hydrogen bonds;

2. D = deoxyribose;

Ignore sugar

3. E = phosphate;

Ignore phosphorus, Ignore molecule

3

(iii)

Name of base	Percentage
Thymine	34
Cytosine / Guanine	16
Adenine	34
Cytosine / Guanine	16

Spelling must be correct to gain MP1

First mark = names correct

Second mark = % correct, with adenine as 34%

2

(b) (i) 153;

1

(ii) Some regions of the gene are non-coding / introns / start / stop code / triplet / there are two DNA strands;

Allow addition mutation

Ignore unqualified reference to mutation

Accept reference to introns and exons if given together

Ignore 'junk' DNA / multiple repeats

1

[8]

M8. (a) (i) UGC;

1

(ii) TGCTAC;

1

(b) (DNA) contains introns / non-coding bases / mRNA only contains exons / coding bases;

Assume that 'it' refers to DNA

Neutral: DNA contains introns and exons

Neutral: 'splicing'

Neutral: pre-mRNA contains introns

Ignore refs. to start and stop codons

1

(c) Different primary structure / amino acid sequence / amino acid coded for;

Reject: different amino acids produced / formed

Neutral: refs. to bonds

1

(d) 1. Acetylcholine not broken down / stays bound to receptor;

2. Na^+ ions (continue to) enter / (continued) depolarisation / Na^+ channels (kept) open / action potentials / impulses fired (continuously);

3. (Intercostal) muscles stay contracted / cannot relax;

'Muscles contract' is not enough

Accept: diaphragm stays contracted / cannot relax

3

[7]

M9. (a) (i) 9;

Accept: nine

1

(ii) Introns / non-coding DNA / junk DNA;

Start / stop code / triplet;

Neutral: Repeats.

Accept: 'Introns and exons present'.

Reject: 'Due to exons'.

1 max

(b) Change in amino acid / s / primary structure;

Change in hydrogen / ionic / disulfide bonds;

Alters tertiary structure;

Reject: 'Different amino acid is formed' – negates first marking point.

Neutral: Reference to active site.

3

(c) Number of bases

	Number of bases			
	C	G	A	T
Strand A	26	**19**	**20**	**9**
Strand B	19	**26**	9	**20**

Second column correct;

Columns three and four correct;

2

[7]

M10. (a) (i) Phosphate and ribose;

Accept in either order. Both correct for one mark.

For phosphate accept PO_4 */ Pi /* Ⓟ *but not P.*

Do not accept phosphorus.

Ignore references to pentose / sugar.

1

(ii) TAGGCA;

1

(b) (i) Does not contain hydrogen bonds / base pairs / contains codons / does not contain anticodon / straight / not folded / no amino acid binding site / longer;

Assume that "it" refers to mRNA.

Do not accept double stranded.

1

(ii) (pre-mRNA) contains introns / mRNA contains only exons;

Assume that "it" refers to pre-mRNA.

Accept non-coding as equivalent to intron.

1

(c) (i)

Part of chromosome	**U**
Middle	18
End	21

One mark for both figures correct

1

(ii) 1. Have different (base) sequences / combinations of (bases);

2. (Pre-mRNA) transcribed from different DNA / codes for different proteins;

2

[7]

M11. (a) Introns;

1

(b) Ile Gly Val Ser;

1

(c) (i) Has no effect / same amino acid (sequence) / same primary structure;

Q Reject same amino acid formed or produced.

1

Glycine named as same amino acid;

1

It still codes for glycine = two marks.

(ii) Leu replaces Val / change in amino acid (sequence) / primary structure;

Change in hydrogen / ionic bonds which alters tertiary structure / active site;

***Q** Different amino acid formed or produced negates first marking point.*

Substrate cannot bind / no longer complementary / no enzyme-substrate complexes form;

Active site changed must be clear for third marking point but does not need reference to shape.

3

(d) (i) Interphase / S / synthesis (phase);

1

(ii) DNA / gene replication / synthesis occurs / longest stage;

Allow 'genetic information' = DNA.

Allow 'copied' or 'formed' = replication / synthesis

1

[9]